(b) hybridizing the target nucleic acid to the array of probes, wherein the sequence of the target nucleic acid is a variant of the reference sequence and provided the probe array does not contain every possible probe sequence of a given length;

(c) determining the relative hybridization of the probes to the target nucleic acid,

(d) estimating the sequence of the target nucleic acid from the relative hybridization of the probes;

(e) providing a further array of probes comprising a probe set comprising probes complementary to the estimated sequence of the target nucleic acid and provided the further probe array does not contain every possible probe sequence of a given length;

(f) hybridizing the target nucleic acid to the further array of probes;

(g) determining the relative hybridization of the probes to the target nucleic acid;

(h) reestimating the sequence of the target nucleic acid from the relative hybridization of the probes.

Please amend claim 15 as follows:

15.     (Amended) A method of analyzing a target nucleic acid, comprising:

(a) designing an array of probes to be complementary to an estimated sequence of the target nucleic acid provided the array does not contain every possible probe sequence of a given length,

(b) hybridizing the array of probes to the target nucleic acid;

(c) determining a reestimated sequence of the target nucleic acid from the hybridization pattern of the array to the target nucleic acid sequence to; and